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RAW SEQUENCE LISTING

DATE: 01/25/2002

PATENT APPLICATION: US/09/582,337

TIME: 11:56:57

Input Set : A:\Sequence.txt

Output Set: N:\CRF3\01252002\I582337.raw

3 <110> APPLICANT: Japan Tobacco, Inc.  
 5 <120> TITLE OF INVENTION: Monoclonal Antibody Against Connective Tissue Growth Factor  
 6 and Medicinal Uses Thereof  
 8 <130> FILE REFERENCE: J1-009PCT  
 C--> 10 <140> CURRENT APPLICATION NUMBER: US/09/582,337  
 C--> 11 <141> CURRENT FILING DATE: 2000-06-23  
 13 <150> PRIOR APPLICATION NUMBER: JP P1997-367699  
 14 <151> PRIOR FILING DATE: 1997-12-25  
 16 <150> PRIOR APPLICATION NUMBER: JP P1998-356183  
 17 <151> PRIOR FILING DATE: 1998-12-15  
 19 <160> NUMBER OF SEQ ID NOS: 27  
 21 <170> SOFTWARE: PatentIn Ver. 2.0  
 23 <210> SEQ ID NO: 1  
 24 <211> LENGTH: 2338  
 25 <212> TYPE: DNA  
 26 <213> ORGANISM: Rat  
 28 <220> FEATURE:  
 29 <221> NAME/KEY: 5'UTR  
 30 <222> LOCATION: (1)..(212)  
 32 <220> FEATURE:  
 33 <221> NAME/KEY: CDS  
 34 <222> LOCATION: (213)..(1256)  
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 37 <221> NAME/KEY: 3'UTR  
 38 <222> LOCATION: (1257)..(2338)  
 40 <220> FEATURE:  
 41 <221> NAME/KEY: polyA\_signal  
 42 <222> LOCATION: (2297)..(2302)  
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 47 gacggcagca gccccagccc agtggacaac cccaggagcc accacctgga gcgtccggac 120  
 49 accaacctcc gccccgagac cgagtccagg ctccggccgc gcccctcgtc gcctctgcac 180  
 51 cccgctgtgc gtctctctgc cgcgccccga cc atg ctc gcc tcc gtc gcg ggt 233  
 52 Met Leu Ala Ser Val Ala Gly  
 53 1 5  
 55 ccc gtt agc ctc gcc ttg gtg ctc ctc ctc tgc acc cgg cct gcc acc 281  
 56 Pro Val Ser Leu Ala Leu Val Leu Leu Cys Thr Arg Pro Ala Thr  
 57 10 15 20  
 59 ggc cag gac tgc agc gcg cag tgt cag tgc gca cgt gaa gcg gcg ccg 329  
 60 Gly Gln Asp Cys Ser Ala Gln Cys Gln Cys Ala Arg Glu Ala Ala Pro  
 61 25 30 35  
 63 cgc tgc ccc gcc ggc gtg agc ctg gtg ctg gac ggc tgc ggc tgc tgc 377  
 64 Arg Cys Pro Ala Gly Val Ser Leu Val Leu Asp Gly Cys Gly Cys Cys

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65	40		45		50		55	
67	cgc gtc tgc gcc aag cag ctg gga gaa ctg tgc acg gag cgt gat ccc	425						
68	Arg Val Cys Ala Lys Gln Leu Gly Glu Leu Cys Thr Glu Arg Asp Pro							
69			60		65		70	
71	tgc gac cca cac aag ggt ctc ttc tgc gac ttc ggc tcc ccc gcc aac	473						
72	Cys Asp Pro His Lys Gly Leu Phe Cys Asp Phe Gly Ser Pro Ala Asn							
73			75		80		85	
75	cgc aag att ggc gtg tgc cct gcc aaa gat ggt gca ccc tgt gtc ttc	521						
76	Arg Lys Ile Gly Val Cys Pro Ala Lys Asp Gly Ala Pro Cys Val Phe							
77			90		95		100	
79	ggt ggg tcc gtg tac cgc agc ggc gag tcc ttc caa agc agt tgc aaa	569						
80	Gly Gly Ser Val Tyr Arg Ser Gly Glu Ser Phe Gln Ser Ser Cys Lys							
81			105		110		115	
83	tac cag tgc act tgc ctg gat ggg gcc gtg ggc tgt gtg ccc ctg tgc	617						
84	Tyr Gln Cys Thr Cys Leu Asp Gly Ala Val Gly Cys Val Pro Leu Cys							
85	120		125		130		135	
87	agc atg gac gtg cgc ctg ccc agc cct gac tgc ccc ttc ccg aga agg	665						
88	Ser Met Asp Val Arg Leu Pro Ser Pro Asp Cys Pro Phe Pro Arg Arg							
89			140		145		150	
91	gtc aag ctg ccc ggg aaa tgc tgt gag gag tgg gtg tgt gat gag ccc	713						
92	Val Lys Leu Pro Gly Lys Cys Cys Glu Glu Trp Val Cys Asp Glu Pro							
93			155		160		165	
95	aag gac cgc aca gtg gtt ggc cct gcc cta gct gcc tac cga ctg gaa	761						
96	Lys Asp Arg Thr Val Val Gly Pro Ala Leu Ala Ala Tyr Arg Leu Glu							
97			170		175		180	
99	gac aca ttt ggc cct gac cca act atg atg cga gcc aac tgc ctg gtc	809						
100	Asp Thr Phe Gly Pro Asp Pro Thr Met Met Arg Ala Asn Cys Leu Val							
101			185		190		195	
103	cag acc aca gag tgg agc gcc tgt tct aag acc tgt ggg atg ggc atc	857						
104	Gln Thr Thr Glu Trp Ser Ala Cys Ser Lys Thr Cys Gly Met Gly Ile							
105	200		205		210		215	
107	tcc acc cgg gtt acc aat gac aat acc ttc tgc agg ctg gag aag cag	905						
108	Ser Thr Arg Val Thr Asn Asp Asn Thr Phe Cys Arg Leu Glu Lys Gln							
109			220		225		230	
111	agt cgt ctc tgc atg gtc agg ccc tgt gaa gct gac cta gag gaa aac	953						
112	Ser Arg Leu Cys Met Val Arg Pro Cys Glu Ala Asp Leu Glu Glu Asn							
113			235		240		245	
115	att aag aag ggc aaa aag tgc atc cgg acg cct aaa att gcc aag cct	1001						
116	Ile Lys Lys Gly Lys Lys Cys Ile Arg Thr Pro Lys Ile Ala Lys Pro							
117			250		255		260	
119	gtc aag ttt gag ctt tct ggc tgc acc agt gtg aag acc tac cgg gct	1049						
120	Val Lys Phe Glu Leu Ser Gly Cys Thr Ser Val Lys Thr Tyr Arg Ala							
121			265		270		275	
123	aag ttc tgt ggg gtg tgc acg gac ggc cgc tgc aca ccg cac aga	1097						
124	Lys Phe Cys Gly Val Cys Thr Asp Gly Arg Cys Cys Thr Pro His Arg							
125	280		285		290		295	
127	acc acc aca ctg ccg gtg gag ttc aag tgc ccc gat ggc gag atc atg	1145						
128	Thr Thr Thr Leu Pro Val Glu Phe Lys Cys Pro Asp Gly Glu Ile Met							
129			300		305		310	

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131 aaa aag aac atg atg ttc atc aag acc tgt gcc tgc cat tac aac tgt 1193
132 Lys Lys Asn Met Met Phe Ile Lys Thr Cys Ala Cys His Tyr Asn Cys
133          315          320          325
135 ccc ggg gac aat gac atc ttt gag tcc ttg tac tac agg aag atg tat 1241
136 Pro Gly Asp Asn Asp Ile Phe Glu Ser Leu Tyr Tyr Arg Lys Met Tyr
137          330          335          340
139 gga gac atg gcg taa agccaggag taaggagacac gaactcattt agactataac 1296
140 Gly Asp Met Ala
141          345
143 ttgaactgag ttacatctca ttttcttctg taaaaaaaaa aaaaagggtt acagtagcac 1356
145 attaatTTaa atctgggttc ctaactgctg tgggagaaaa caccaccg aagtgagaac 1416
147 cgtgtgtcat tgtcatgcaa atagcctgtc aatctcagac actggtttcg agacagtTTa 1476
149 gacttgacag ttgttcaacta gcgcacagtg acagaacgca cactaagggtg agcctcctgg 1536
151 aagagtggag atgccaggag aaagacaggt actagctgag gtcattTTaa aagcagcgat 1596
153 atgcctactt ttggagtggt gacaggggag ggacattata gcttgcttgc agacagacct 1656
155 gctctagcaa gagctgggtg tgtgtcctcc actcggtgag gctgaagcca gctattcttt 1716
157 cagtaagaac agcagtttca gcgctgacat tctgattcca gygacactgg tcgggagTca 1776
159 gaaccttgTc tattagactg gacagcttgt ggcaagtGaa ttgcccgtta acaagccaga 1836
161 tttttatgga tcttgtaaat attgtggata aatatatata tttgtacagt tatctargtt 1896
163 aattttaaaga cgtttTgtgcc tattgttctt gttttaagtT cttttggaat ttttaaaactg 1956
165 atagcctcaa actccaaaca ccatcgatag gacataaagc ttgtctgtga ttcaaaacaa 2016
167 aggagatact gcagtggaaa ctgtaacctg agtgactgtc tgtcagaaca tatggtacgt 2076
169 agacggtaaa gcaatggatc agaagtcaga tttctagtag gaaatgtaaa atcactgttg 2136
171 gcgaacaaat ggcctttatt aagaaatggc ttgctcaggg taactggtca gatttccacg 2196
173 aggaagtgtt tgctgcttct ttgactatga ctggtttggg aggcagttta tttgttgaga 2256
175 gtgtgaccaa aagttacatg ttTgcacctt tctagttgaa aataaagtat atatatTTTT 2316
177 tatatgaaaa aaaaaaaaaa aa 2338
180 <210> SEQ ID NO: 2
181 <211> LENGTH: 347
182 <212> TYPE: PRT
183 <213> ORGANISM: Rat
185 <400> SEQUENCE: 2
186 Met Leu Ala Ser Val Ala Gly Pro Val Ser Leu Ala Leu Val Leu Leu
187 1 5 10 15
189 Leu Cys Thr Arg Pro Ala Thr Gly Gln Asp Cys Ser Ala Gln Cys Gln
190 20 25 30
192 Cys Ala Arg Glu Ala Ala Pro Arg Cys Pro Ala Gly Val Ser Leu Val
193 35 40 45
195 Leu Asp Gly Cys Gly Cys Cys Arg Val Cys Ala Lys Gln Leu Gly Glu
196 50 55 60
198 Leu Cys Thr Glu Arg Asp Pro Cys Asp Pro His Lys Gly Leu Phe Cys
199 65 70 75 80
201 Asp Phe Gly Ser Pro Ala Asn Arg Lys Ile Gly Val Cys Pro Ala Lys
202 85 90 95
204 Asp Gly Ala Pro Cys Val Phe Gly Gly Ser Val Tyr Arg Ser Gly Glu
205 100 105 110
207 Ser Phe Gln Ser Ser Cys Lys Tyr Gln Cys Thr Cys Leu Asp Gly Ala
208 115 120 125
210 Val Gly Cys Val Pro Leu Cys Ser Met Asp Val Arg Leu Pro Ser Pro

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211      130      135      140
213 Asp Cys Pro Phe Pro Arg Arg Val Lys Leu Pro Gly Lys Cys Cys Glu
214 145      150      155      160
216 Glu Trp Val Cys Asp Glu Pro Lys Asp Arg Thr Val Val Gly Pro Ala
217      165      170      175
219 Leu Ala Ala Tyr Arg Leu Glu Asp Thr Phe Gly Pro Asp Pro Thr Met
220      180      185      190
222 Met Arg Ala Asn Cys Leu Val Gln Thr Thr Glu Trp Ser Ala Cys Ser
223      195      200      205
225 Lys Thr Cys Gly Met Gly Ile Ser Thr Arg Val Thr Asn Asp Asn Thr
226      210      215      220
228 Phe Cys Arg Leu Glu Lys Gln Ser Arg Leu Cys Met Val Arg Pro Cys
229 225      230      235      240
231 Glu Ala Asp Leu Glu Glu Asn Ile Lys Lys Gly Lys Lys Cys Ile Arg
232      245      250      255
234 Thr Pro Lys Ile Ala Lys Pro Val Lys Phe Glu Leu Ser Gly Cys Thr
235      260      265      270
237 Ser Val Lys Thr Tyr Arg Ala Lys Phe Cys Gly Val Cys Thr Asp Gly
238      275      280      285
240 Arg Cys Cys Thr Pro His Arg Thr Thr Thr Leu Pro Val Glu Phe Lys
241      290      295      300
243 Cys Pro Asp Gly Glu Ile Met Lys Lys Asn Met Met Phe Ile Lys Thr
244 305      310      315      320
246 Cys Ala Cys His Tyr Asn Cys Pro Gly Asp Asn Asp Ile Phe Glu Ser
247      325      330      335
249 Leu Tyr Tyr Arg Lys Met Tyr Gly Asp Met Ala
250      340      345
253 <210> SEQ ID NO: 3
254 <211> LENGTH: 20
255 <212> TYPE: DNA
256 <213> ORGANISM: Artificial Sequence
258 <220> FEATURE:
259 <223> OTHER INFORMATION: Description of Artificial Sequence: Artificially
260 synthesized primer sequence
262 <220> FEATURE:
263 <221> NAME/KEY: primer_bind
264 <222> LOCATION: (1)..(20)
266 <400> SEQUENCE: 3
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270 <210> SEQ ID NO: 4
271 <211> LENGTH: 21
272 <212> TYPE: DNA
273 <213> ORGANISM: Artificial Sequence
275 <220> FEATURE:
276 <223> OTHER INFORMATION: Description of Artificial Sequence: Artificially
277 synthesized primer sequence
279 <220> FEATURE:
280 <221> NAME/KEY: primer_bind
281 <222> LOCATION: (1)..(21)

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283 <400> SEQUENCE: 4
284 gcacaggtct tgatgaacat c 21
287 <210> SEQ ID NO: 5
288 <211> LENGTH: 444
289 <212> TYPE: DNA
290 <213> ORGANISM: Homo sapiens
292 <220> FEATURE:
293 <221> NAME/KEY: CDS
294 <222> LOCATION: (1)..(444)
296 <220> FEATURE:
297 <221> NAME/KEY: sig_peptide
298 <222> LOCATION: (1)..(57)
300 <220> FEATURE:
301 <221> NAME/KEY: V_region
302 <222> LOCATION: (58)..(363)
304 <400> SEQUENCE: 5
305 atg gag ttt ggg ctg agc tgg att ttc ctt gct gct att tta aaa ggt 48
306 Met Glu Phe Gly Leu Ser Trp Ile Phe Leu Ala Ala Ile Leu Lys Gly
307 1 5 10 15
309 gtc cag tgt gag gtg cag ctg gtg gag tct ggg gga ggc ttg gta aag 96
310 Val Gln Cys Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys
311 20 25 30
313 cct ggg ggg tcc ctt aag acc tct cct gtg cag cct ctg gat tca act 144
314 Pro Gly Gly Ser Leu Lys Thr Ser Pro Val Gln Pro Leu Asp Ser Thr
315 35 40 45
317 ttc agt aac gcc tgg atg agc tgg gtc cgc cag gct cca gga agg ggc 192
318 Phe Ser Asn Ala Trp Met Ser Trp Val Arg Gln Ala Pro Gly Arg Gly
319 50 55 60
321 tgg agt ggg ttg gcc gta tta aaa gca aaa ctg atg gtg gga cac aca 240
322 Trp Ser Gly Leu Ala Val Leu Lys Ala Lys Leu Met Val Gly His Thr
323 65 70 75 80
325 gac tac gct gca ccc gtg aaa ggc aga ttc acc atc tca aga gat gat 288
326 Asp Tyr Ala Ala Pro Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp
327 85 90 95
329 tca aaa aac acg ctg tat ctg caa atg aac agc ctg aaa acc gag gac 336
330 Ser Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Lys Thr Glu Asp
331 100 105 110
333 aca gcc gtg tat tac tgt acc aca aaa tgg gtg gct acg gac tac ttt 384
334 Thr Ala Val Tyr Tyr Cys Thr Thr Lys Trp Val Ala Thr Asp Tyr Phe
335 115 120 125
337 gac tac tgg ggc cag gga acc ctg gtc acc gtc tcc tca gcc tcc acc 432
338 Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr
339 130 135 140
341 aag ggc cca tcg 444
342 Lys Gly Pro Ser
343 145
346 <210> SEQ ID NO: 6
347 <211> LENGTH: 148
348 <212> TYPE: PRT

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VERIFICATION SUMMARY

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Input Set : A:\Sequence.txt

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L:10 M:270 C: Current Application Number differs, Replaced Application Number

L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date